

75703

STIC-Biotech/ChemLib

From: Gibbs, Terra
Sent: Friday, September 13, 2002 1:41 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search

Could you please search SEQ ID NO: 3 of serial number 10/003354

Please do a length limited search of 50 nucleotides or less. Also no EST's.

Terra Gibbs #79523
AU 1635
Mailbox 11E12
306-3221

THANK YOU!

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 9/14/02
Date Completed: 9/18/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: 1
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: W1
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 22:59:43 : Search time 4476.82 Seconds
(without alignments)
17356.121 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attacagcgccgtgttagt.....aaacttaagtattatta 3713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_sy:*
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No. Query Score Match Length DB ID Description

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23	20.4	0.5	50	6	AX160060	AX160060 Sequence
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25	20.2	0.5	40	6	AX299737	AX299737 Sequence
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28	20.2	0.5	46	6	I42426	I42426 Sequence 17
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40	20.2	0.5	50	6	I29704	I29704 Sequence 57
41	20.2	0.5	50	6	I29705	I29705 Sequence 57
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43	20.2	0.5	50	6	I91258	I91258 Sequence 45
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45	20.2	0.5	50	6	I91379	I91379 Sequence 57

ALIGNMENTS

RESULT 1
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LOCUS A59476 49 bp DNA
DEFINITION Sequence 26 from Patent WO9705234.
ACCESSION A59476
VERSION A59476.1 GI:3714788
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS Chamberlain, S., Pook, M.A., Doudney, C., William, E., Hillermann, R.,
TITLE Garcia-Valdecasas, J.J. and C.
JOURNAL GENE FOR FRIEDREICH'S ATAXIA
Patent: WO 9705234-A 26 13-FEB-1997;
IMPERIAL COLLEGE (GB)
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1. 49
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ORIGIN


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RESULT 5
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LOCUS AB4538 35 bp DNA linear PAT 21-JUN-2000
DEFINITION Sequence 10 from Patent WO9845476.
ACCESSION AB4538
VERSION AB4538.1 GI:6733457
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
SUBSTANCE
Patent: WO 9845476-A 10 15-OCT-1998;
INST OF FOOD RESEARCH (GB); SCHWEITZER MICHAEL (GB)
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source
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Db 33 CCGGCGCTTTTCTTTTCTTTTCTTCGAA 3

RESULT 6
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LOCUS AX352053 38 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 349 from Patent WO0193902.
ACCESSION AX352053
VERSION AX352053.1 GI:18617336
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/note="Synthetic HDR"
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LOCUS AX159492 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2820 from Patent WO0140521.
ACCESSION AX159492
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VERSION AX159492.1 GI:14540823
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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1. .50
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25. .26
/note="Nucleotide deleted between bases 25 and 26"
Accession number c942513366"
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RESULT 8
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LOCUS AX159494 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2822 from Patent WO0140521.
ACCESSION AX159494
VERSION AX159494.1 GI:14540825
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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ORIGIN

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Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2564 agcttcctctctctctctctctgaaaaag 2597
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Db 2 AGTTGCTTTTGTTTCTTTTAAAGACAGG 35
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LOCUS	AX159496	50 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence	2824	from Patent	WO0140521.	
ACCESSION	AX159496				
VERSION	AX159496.1	GI:14540827			
KEYWORDS	human.				
SOURCE	Organism	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 50)				
AUTHORS	Shimkets,R.A. and Leach,M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
JOURNAL	Patent: WO 0140521-A 2824 07-JUN-2001;				
FEATURES	Curagen Corporation (US);				
source	Location/Qualifiers				
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	/db_xref="taxon:9606"				
misc_feature	25..26				
	/note="Nucleotide deleted between bases 25 and 26				
	Accession number cg42513366"				
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	/note="2 of 2 allelic variants (2823 is other entry)"				
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	Matches 26;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
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LOCUS	AR069130/c				
DEFINITION	AR069130	43 bp	DNA	linear	PAT 18-FEB-2000
ACCESSION	AR069130	Sequence 14 from patent US 5891439.			
VERSION	AR069130.1	GI:7220018			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 43)				
AUTHORS	Valdya,T., Bahkiet,A., Olsson,T., Kristensson,K. and Donelson,J.E.				
TITLE	Lymphocyte stimulating factor				
JOURNAL	Patent: US 5891439-A 14 06-APR-1999;				
FEATURES	Location/Qualifiers				
source	1..43				
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Best Local Similarity	73.0%:	Pred. No.	2e+06:	
Matches	27:	Conservative	0:	Mismatches 10:
				Indels 0:
				Gaps 0:
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Db	42	TTTTTTTTTTTTTTTTTTTAGTGAATGACATAAAG	6	
RESULT	11			
AXI72348				
LOCUS	AXI72348	45 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO0144811.			PAT 03-JUL-2001

ACCESSION	AX172348	GI:14597500
VERSION	AX172348.1	
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS	Singh,S., Pease,J.S., Sadakian,J., Wagner,D.B. and Ullman,E.F.	
TITLE	Light-emitting particles for diagnostic and therapeutic use	
JOURNAL	Patent: WO 0144811-A 1 21-JUN-2001;	
	DADE BEHRING INC. (US)	
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source	1..45	location/Qualifiers
	/organism="synthetic construct"	
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	/note="Oligonucleotide probe"	
BASE COUNT	11 a	3 c
ORIGIN		6 g
		25 t

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Matches	30;	Conservative	0; Mismatches 15; Indels 0; Gaps 0;
QY	2568	tctctctctcttcttcttcttctgaagaaaggaacacacagca	2612
DB	1	TTTTTTTTTTTTTTTTTTTTTTGTTAAAGAGACCCTTCATGAGGA	45

RESULT	12				
LOCUS	132124				
DEFINITION	Sequence 14 from patent US 5585242.	32 bp	DNA	linear	PAT 06-FEB-1997
ACCESSION	132124				
VERSION	132124.1	GI:1822915			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 32)				
TITLE	Bouma,S.R., Khalil,O.S. and Pablich,E.K.				
	Method for detection of nucleic acid using total internal reflectance				
JOURNAL	Patent: US 5585242-A 14 17 -DEC-1996;				
FEATURES	Location/Qualifiers				
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ORIGIN					

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QY	2555	ccacctccacgctctctctctctctctttttt	2586	
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RESULT	13			
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LOGS		AX161426	50 bp	DNA
DEFINITION		Sequence	4754 from Patent WO0140521.	linear
ACCESSION		AX161426		
VERSION		AX161426.1	GI:14542757	
KEYWORDS				
SOURCE		human.		
ORGANISM		Homo sapiens		
		Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1. (bases 1 to 50)		
AUTHORS		Shimkets, R.A. and Leach, M.		

TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
JOURNAL	Patent: WO 0140521-A 4/54 07 -JUN-2001; Curagen Corporation (US)				
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Oy	3682 ttctaatgtaataacttaagtactttta 3713				
Db	50 TTTTCTGCAGCAACTTATGACTTTTTA 19				
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LOCUS	AX199596	50 bp	DNA	linear	PAT 29-AUG-2001
DEFINITION	Sequence 526 from Patent WO0151670.				
ACCESSION	AX199596				
VERSION	AX199596.1 GI:15390030				
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
REFERENCE	1 (bases 1 to 50)				
ADTHORS	Shimkets, R.A. and Leach, M.D.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
JOURNAL	Patent: WO 0151670-A 526 19-JUL-2001; Curagen Corporation (US)				
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Db	48 GAGTTTCATCTTCTGACCAGATGACACCAATTTTGCACTTTTCTG 1				
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DEFINITION	Sequence 10 from Patent WO0063365.				
ACCESSION	AX040470				
VERSION	AX040470.1 GI:11230262				
KEYWORDS	synthetic construct.				
SOURCE					

ORGANISM	synthetic construct artificial sequence.			
REFERENCE	1 (bases 1 to 41)			
AUTHORS	Belotserkovskii, B., Reddy, G. and Zarling, D.			
TITLE	Locked nucleic acid hybrids and methods of use			
JOURNAL	Patent: WO 0063365-A 10 26-Oct-2000; Pangene Corporation (US)			
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Job time: 8162 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 23:03:38 : Search time 382.89 Seconds
(without alignments)
16649.438 Million cell updates/sec

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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	22.6	0.6	40	22	AA173161
7	22.2	0.6	40	22	AAH20340
8	22.2	0.6	48	22	AA130218
9	22.2	0.6	50	16	AA087804

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14	21.6	0.6	50	22	AA131293	Human SNP oligonuc
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16	21.2	0.6	47	22	AA130217	Human SNP oligonuc
17	21.2	0.6	50	22	AA127921	Human SNP oligonuc
18	21.2	0.6	50	22	AA128580	Human SNP oligonuc
19	21.2	0.6	50	22	AA175879	Human silent SNP c
20	21.2	0.6	50	22	AA175881	Human silent SNP c
21	21.2	0.6	50	22	AA175883	Human silent SNP c
22	21	0.6	44	22	AA128737	Human SNP oligonuc
23	21	0.6	45	20	AA231524	Probe for HIV RNA
24	21	0.6	45	20	AA211012	Probe #1 for HIV t
25	21	0.6	45	22	AA18751	Probe #1 used for
26	21	0.6	46	20	AA177169	Chimeric packaging
27	20.8	0.6	47	21	AA267568	Human map-related
28	20.8	0.6	50	22	AA128914	Human SNP oligonuc
29	20.8	0.6	50	22	AA177813	Human silent SNP c
30	20.8	0.6	50	22	AAH89745	Human coding sequ
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33	20.6	0.6	45	16	AA080709	Drosophila hsp70 g
34	20.6	0.6	45	22	AA128913	S. cerevisiae YKR0
35	20.6	0.6	47	21	AA267569	Human map-related
36	20.6	0.6	48	22	AAH97394	Human Chk1 ribozym
37	20.6	0.6	50	22	AA129036	Human SNP oligonuc
38	20.6	0.6	50	22	AA130220	Human SNP oligonuc
39	20.6	0.6	50	23	AB100059	Human silent nonco
40	20.4	0.5	40	15	AA055168	Sequence of primer
41	20.4	0.5	41	20	AA344851	Primer for adapter
42	20.4	0.5	41	20	AA23455	Human neutrophil c
43	20.4	0.5	46	24	AA595733	Allele discriminat
44	20.4	0.5	47	21	AA267078	Human map-related
45	20.4	0.5	47	21	AA267213	Human map-related

ALIGNMENTS

RESULT 1	
ID	AA184374 standard; DNA; 49 Bp.
AC	AA184374;
XX	
DT	12-NOV-1997 (first entry)
XX	
DE	Friedreich's ataxia STM7 gene exon 11.
XX	
KW	STM7, I gene; Friedreich's ataxia; FRDA; neurodegeneration;
KW	phosphatidylinositol-4-phosphate 5-kinase; Ptdinspk;
KW	transgenic animal; animal model; diagnosis; therapy;
KW	STM7, IITa; STM7, IITb; STM7, IITc; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9705234-A2.
XX	
PD	13-FEB-1997.
XX	
PF	24-JUL-1996; 96WO-GB01786.
XX	
PR	28-JUL-1995; 95GB-0015508.
XX	
PR	26-JUL-1995; 95GB-0015309.
XX	
PA	(UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
XX	
PI	Chamberlain S, Doudney CWE, Garcia-Valdecasas JJC;
XX	Hillermann R, Pook MA;
XX	
DR	WPI; 1997-145674/13.

XX New gene, *STM7*, and new protein causing Friedreich's Ataxia -
 PT encodes phosphatidylinositol phosphate isozyme; also splice
 PT variants and transgenic animals, for diagnosing pre-disposition to
 PT Friedreich's ataxia
 XX
 PS Claim 1; Fig 16; 82pp; English.
 XX
 CC DNA sequences (AA184364-86) are provided for exons 1-23,
 CC respectively, of the human *STM7* gene associated with Friedreich's
 CC ataxia (FRDA). The *STM7*.1 gene (see AA184358) comprises exons
 CC 1-16 of the gene, while splice variant *STM7*.111a includes exons
 CC 1-13, 17 and 19-22, splice variant *STM7*.111b includes exons
 CC 1-13, 17, 19, 21-22 and splice variant *STM7*.111c includes exons
 CC 1-15 and 19-22. *STM7* nucleic acids can be used to produce *STM7*
 CC polypeptides (see AA000978) in transfected host cells, to design
 CC probes (esp. oligonucleotides) from exons 1-16, partic. 7-11) used
 CC in a claimed method for determining an inherited predisposition to
 CC FRDA, to generate transgenic animal models of FRDA and in somatic
 CC cell therapy.
 CC
 SQ Sequence 49 BP; 15 A; 5 C; 13 G; 16 T; 0 other;
 XX
 XX Query Match 0.8%; Score 28.8; DB 18; Length 49;
 Best Local Similarity 75.0%; Pred. No. 4e+02;
 Matches 36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 OY 1591 gttgttaagaagtgtgagcactcttgaaagccctgtatcatgacgg 1638
 DB 1 gtaataagaagaagttagaacattctcttgaaagccctgtatcatgacg 48
 XX
 RESULT 2
 ID AAL30887/c
 AC AAL30887 standard; DNA; 50 BP.
 XX
 AC AAL30887;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #4095.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200147944-A2.
 PN
 PD 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000MO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 PI
 DR WPI; 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 2809; 4143pp; English.

PS Claim 1; Page 2562; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amyloses, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 50 BP; 16 A; 3 C; 6 G; 25 T; 0 other;
 XX
 XX Query Match 0.7%; Score 24.8; DB 22; Length 50;
 Best Local Similarity 72.7%; Pred. No. 5.5e+03;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 OY 2577 ttttttttctgaaaaaagacacacacacacattt 2620
 DB 44 TCTTTTAAAAAAGCAAAAGCATATACACATATT 1
 XX
 RESULT 3
 ID AAL31735
 AC AAL31735 standard; DNA; 50 BP.
 XX
 AC AAL31735;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #4943.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200147944-A2.
 PN
 PD 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000MO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 PI
 DR WPI; 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 2809; 4143pp; English.

[illegible]

CC	intracellular availability of the TA. The conjugates of the invention
CC	are used to inhibit cell proliferation in cells carrying the
CC	particular growth factor receptor; also when TA is DNA it can be used
CC	to deliver this to cells (for gene therapy). A specific application
CC	is to prevent excessive proliferation of epithelial cells,
CC	fibroblasts and keratinocytes in the anterior eye after surgery,
CC	partic. to prevent recurrence of pterygia after surgical removal,
CC	closure of trabeculectomy after glaucoma surgery and corneal clouding
CC	after excimer laser treatment. Other conditions which may be treated
CC	include tumours, restenosis, psoriasis, Dupuytren's contracture,
CC	diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.
XX	
SO	Sequence 45 BP; 2 A; 16 C; 17 G; 10 T; 0 other;
XX	
Query Match	0.6%; Score 22.6; DB 16; Length 45;
Best Local Similarity	75.7%; Pred. No. 2.2e+04;
Matches 28; Conservative	0; Mismatches 9; Indels 0; Gaps 0;
Oy	401 atggcgtcgccctccctccgcgcgtcttcgtcgcg 437
Db	3 atggcctcgtcgtcgtcgcgcgtcgtcgtcgcgcg 39
XX	
RESULT 5	
ID	AAA12866
XX	AAA12866 standard; DNA; 45 BP.
AC	AAA12866;
XX	
DT	18-JUL-2000 (first entry)
XX	
DE	DNA encoding (Ser4-Gly)2 flexible linker peptide, SEQ ID NO:50.
XX	
KW	Targetted gene delivery; fibroblast growth factor receptor;
KW	FGFR-binding protein; nucleic acid binding protein;
KW	receptor-internalised ligand; cytotoxin; saprolin; gene therapy;
KW	cytoid; antiproliferative; cancer; melanoma; diabetic retinopathy;
KW	rheumatoid arthritis; restenosis, Dupuytren's contracture; psoriasis;
KW	eczema; nuclear translocation signal; MTS;
KW	cytoplasmic translocation signal; endosome-disruptive peptide; ss.
XX	
OS	Synthetic.
XX	
PN	US6037329-A.
XX	
PD	14-MAR-2000.
XX	
PF	24-SEP-1996; 96US-0718904.
XX	
PR	15-MAR-1994; 94US-0213446.
PR	15-MAR-1994; 94US-0213447.
PR	29-AUG-1994; 94US-0287961.
PR	13-SEP-1994; 94US-0305771.
PR	16-MAY-1995; 95US-0441979.
XX	
PA	(SELE-) SELECTIVE GENETICS INC.
XX	
PI	Chandler LA, Sosnowski BA, Baird JA;
XX	
DR	WPI; 2000-292008/25.
XX	
PT	Gene delivery system, useful for treating or preventing cancer and
PT	rheumatoid arthritis, comprises receptor-internalized ligand linked to
XX	nucleic acid binding domain and nucleic acid -
XX	
PS	Claim 21; Column 33; 131pp; English.
XX	
CC	The invention relates to a novel gene delivery composition for the
CC	targetted delivery of cytotoxins or prodrug-converting enzymes to
CC	proliferating cells. The gene delivery composition comprises a protein
CC	that binds the fibroblast growth factor receptor (FGFR) which is fused
CC	or chemically conjugated to a nucleic acid binding domain. The nucleic

SQ Sequence 45 BP; 2 A; 16 C; 17 G; 10 T; 0 other;

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best local similarity      78.0%   (2001 nt) 2126 nt
Matches    28; Conservative    0; Mismatches    9; Indels    0; Gaps    0;
```

Db 3 atggcctcgtcgtcgtcggcctcgtcgtcgtcggcg 39

AAI73161 standard; DNA; 50 BP.

AC AAI73161;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:102.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US32758.

PR 30-NOV-1999; 99US-0168138.

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25 WPT: 2001-3EE6160/237

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PT therapy -

PS Claim 1; Page 85; 2653pp; English.

AA
CC
CC
sequences (I), which contain single nucleotide polymorphisms (SNPs).

Sequence 50 BP; 8 A; 10 C; 3 G; 29 T; 0 other;

Matches	28;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Db
1 ttcttgcttcttttcttttttcataacaag 37

AAH20340 standard; DNA; 40 BP.

AA AAH20340; AC

DT 01-AUG-2001 (first entry)

DE HHV6 virus p41 gene specific primer p41FH92 SEQ ID 21.

Primer; solid phase amplification of DNA template; SPADT; detection; RGP;

XX

05 Synthetic.

PN US6221635-B1

PD 24-APR-2001.

PF 06-MAY-1999; 99US-0306290.

PR 06-MAY-1999; 99US-0306290.

PA (WIST-) WISTAR INST

PI Rovera G, Mukhopadhyay S,

DR WPJ; 2001-315577/33

PT Detecting the presence of a specific nucleic acid in a sample

presence of genes or gene fam

XX Columns 39: 4000: English

AA This invention relates to a method for detecting the presence of a
CC specific nucleic acid in a sample containing DNA. The method comprises
CC performing solid phase amplification of DNA template (SPART). 5' and 3'
CC primers are irreversibly bound to a solid support, and the DNA from a
CC sample is absorbed and reversibly bound, incubated under amplification
CC reaction conditions and the presence of the specific target DNA is

Human SNP oligonucleotide #7280.

KW Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;

KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN M0200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000MO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 1988; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
CC
XX
SQ Sequence 50 BP; 13 A; 11 C; 14 G; 12 T; 0 other;
Query Match 0.6%; Score 21.8; DB 22; Length 50;
Best Local Similarity 78.8%; Pred. No. 3.9e+04;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2007 ccttgaaagccttgaaagtcagagtcagagtc 2039
Db 15 ccttgaaagcgcgcaagtccttaccgcagtc 47
RESULT 13
AAH20339
ID AAH20339 standard; DNA: 40 BP.
XX
AC AAH20339;
XX
DT 01-AUG-2001 (first entry)
XX
DE HHV6 virus p41 gene specific primer p41FH46 SEQ ID 20.
XX
KW Primer: solid phase amplification of DNA template; SPADP; detection; RGP;
KW genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX

OS Human herpesvirus 6.
OS Synthetic.
XX
PN U56221635-B1.
XX
PD 24-APR-2001.
XX
PF 06-MAY-1999; 99US-0306290.
XX
PR 06-MAY-1999; 99US-0306290.
XX
PA (WIST-) WISTAR INST.
XX
PI Rovera G, Mukhopadhyay S;
XX
DR WPI; 2001-315577/33.
XX
PT Detecting the presence of a specific nucleic acid in a sample
PT containing DNA, useful in scanning large genomic fragments for the
PT presence of genes or gene families, comprises performing solid phase
PT amplification of DNA template -
XX
PS Example 2; Column 28; 49pp; English.
XX
CC This invention relates to a method for detecting the presence of a
CC specific nucleic acid in a sample containing DNA. The method comprises
CC performing solid phase amplification of DNA template (SPADP). 5' and 3'
CC primers are irreversibly bound to a solid support, and the DNA from a
CC sample is absorbed and reversibly bound, incubated under amplification
CC reaction conditions and the presence of the specific target DNA is
CC detected. The method is useful for detecting the presence of a specific
CC nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC cell. SPADP may be used for scanning large genomic fragments for the
CC presence of genes or gene families, or for bacterial diagnostics by
CC examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC for the presence of viral nucleic acid sequences in a sample. SPADP may
CC also be used in forensic medicine by detecting and identifying species
CC specific sequences or for the presence of major histocompatibility
CC complex. The present sequence represents a primer specific for the human
CC herpesvirus 6 (HHV6) p41 gene. The primer is used in an example
CC illustrating the method of the invention.
CC
XX
SQ Sequence 40 BP; 9 A; 3 C; 7 G; 21 T; 0 other;
Query Match 0.6%; Score 21.6; DB 22; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.9e+04;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2567 ttctctctcttttttttcttgaaaggaagaa 2602
Db 1 ttctctctcttttttttcttggaacatagagaa 36
RESULT 14
AAL31293/C
ID AAL31293 standard; DNA: 50 BP.
XX
AC AAL31293;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4501.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX

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```
? TITLE OF INVENTION: PRD1-CATALYZED DNA REPLICATION SYSTEMS
? NUMBER OF SEQUENCES: 89
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Cahill, Sutton & Thomas
? STREET: 155 Park One, 2141 E. Highland Ave.
? CITY: Phoenix
? STATE: Arizona
? COUNTRY: U.S.A.
? ZIP: 85016
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
? COMPUTER: Packard Bell (IBM PC/AT compatible)
? OPERATING SYSTEM: MS-Dos, Version 5.0
? SOFTWARE: Wordperfect Version 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/208,486
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/869,916
? FILING DATE: April 14, 1992
? APPLICATION NUMBER: Japan 240525/91
? FILING DATE: August 26, 1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Janelle Faunce Raupp
? REGISTRATION NUMBER: 30,485
? REFERENCE/DOCKET NUMBER: #3954-A-7
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (602) 956-7000
? TELEFAX: (602) 495-9475
? INFORMATION FOR SEQ ID NO: 57:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 40 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: Other nucleic acid (synthetic DNA)
? US-08-208-486-57

Query Match 0.5%; Score 20.2; DB 1; Length 40;
Best Local Similarity 75.8%; Pred. No. 8.2e+03;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 122 gctactctctctggaagggaagatcccc 154
Db 33 gcttagtcttggggaggggacgatatcccc 1

RESULT 12
? US-08-284-784-17
? Sequence 17, Application US/08284784
? Patent No. 5629172
? GENERAL INFORMATION:
? APPLICANT: MASCARENHAS, DESMOND
? APPLICANT: ZHANG, YANG
? APPLICANT: OLSEN, PAMELA S.
? APPLICANT: OLSEN, DAVID R.
? APPLICANT: CARRILLO, PEDRO A.
? TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
? TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES
? NUMBER OF SEQUENCES: 44
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 755 Page Mill Road
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
? ZIP: 94304-1018
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
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? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/284,784
? FILING DATE: 02-AUG-1994
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: PARK, FREDIE K.
? REGISTRATION NUMBER: 35,636
? REFERENCE/DOCKET NUMBER: 22095-20275.20
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 813-5600
? TELEFAX: (415) 494-0792
? SEQUENCE CHARACTERISTICS:
? LENGTH: 46 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-284-784-17

Query Match 0.5%; Score 20.2; DB 1; Length 46;
Best Local Similarity 68.3%; Pred. No. 9.1e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 132 cctgagtgccttttttggatgctgacatgtaacgctct 1272
Db 6 ccttcgtctcttccatgaggggtgacctggcgcaaatatc 46

RESULT 13
? US-08-854-811-17
? Sequence 17, Application US/08854811
? Patent No. 5914254
? GENERAL INFORMATION:
? APPLICANT: Mascarenhas, Desmond
? APPLICANT: Zhang, Yang
? APPLICANT: Olson, Pamela S.
? APPLICANT: OLSEN, DAVID R.
? APPLICANT: Cohen, Pedro A.
? TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
? TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER
? NUMBER OF SEQUENCES: 49
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 755 PAGE MILL ROAD
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304-1018
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM compatible
? OPERATING SYSTEM: Windows
? SOFTWARE: FastSeq for Windows Version 2.0b
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/854,811
? FILING DATE: 12-MAY-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/284,784
? FILING DATE: 02-AUG-1994
? APPLICATION NUMBER: 08/100,744
? FILING DATE: 02-AUG-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Buffinger, Nicholas S
? REGISTRATION NUMBER: 39,124
? REFERENCE/DOCKET NUMBER: 22095-20275.21
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-813-5600
? TELEFAX: 650-494-0792
```

TELEX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-854-811-17

Query Match
Best Local Similarity 68.3%; Pred. No. 9, 1e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1232 cctgtagtcttcttcttgatgctgacatgtacaacgcctc 1272
Db 6 CCTCTGCTCTTTCATGGTGGTGCACCTGGCAAGATCT 46

RESULT 14
US-08-171-389-456/C
Sequence 456, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 456:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human beta-LH gene
US-08-171-389-456

Query Match
Best Local Similarity 63.3%; Pred. No. 9, 6e+03;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2225 tctcttcctccatgaatggccttagtgcctcagagatggagaccgc 2273
Db 49 TCCCTCGCCCTGCTATGCTTATACCTCGGGTGTGGGGCGCGC 1

RESULT 15
US-08-171-389-576
Sequence 576, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 576:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Adenovirus type-2 IX (start site
INDIVIDUAL ISOLATE: 3575)
US-08-171-389-576

Query Match 0.5%; Score 20.2; DB 1; Length 50;
Best Local Similarity 75.8%; Pred. No. 9.6e+03;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3541 ttagggttgagggaatatattgaggaggct 3573
||| ||||| ||||| ||| ||| |
Db 3 TTAAGGCTGGGAAAGAATATATAAGTGGGGCT 35

Search completed: September 18, 2002, 00:00:45
Job time: 5692 sec

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1  PRIOR APPLICATION NUMBER: 60/091,170
2
3  PRIOR FILING DATE: 1998-06-30
4
5  NUMBER OF SEQ ID NOS: 5662
6
7  SOFTWARE: PatentIn Ver. 2.0
8
9  SEQ ID NO 4074
10
11  LENGTH: 50
12
13  TYPE: DNA
14
15  ORGANISM: Homo sapiens
16
17  FEATURE:
18
19  NAME/KEY: misc feature
20
21  LOCATION: (38)
22
23  OTHER INFORMATION: n equals a,t,g, or c
24
25  NAME/KEY: misc feature
26
27  LOCATION: (40)
28
29  OTHER INFORMATION: n equals a,t,g, or c
30
31  NAME/KEY: misc feature
32
33  LOCATION: (47)
34
35  OTHER INFORMATION: n equals a,t,g, or c
36
37  NAME/KEY: misc feature
38
39  LOCATION: (48)
40
41  OTHER INFORMATION: n equals a,t,g, or c
42
43  OS=342-217A-4074

```

```
-Query Match      0.7%   Score 20.4; DB 17; Length 50;
Best Local Similarity 73.7%; Pred. No. 2e+05;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```

1 RESULT 5
2 US-09-755-374A-17699
3 Sequence 17699, Application US/09755374A
4 GENERAL INFORMATION:
5 APPLICANT: Leach, Martin
6 APPLICANT: Shinkets, Richard A.
7 TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meth
8 TITLE OF INVENTION: Use Thereof
9 FILE REFERENCE: 15966-611
10 CURRENT APPLICATION NUMBER: US/09/755, 374A
11 CURRENT FILING DATE: 2001-01-08
12 PRIOR APPLICATION NUMBER: 60/174962
13 PRIOR FILING DATE: 2000-01-07
14 NUMBER OF SEQ. ID NOS: 28742
15 SEQ ID NO 17699
16 LENGTH: 50
17 TYPE: DNA
18 ORGANISM: Homo sapiens
19 FEATURE:
20 NAME/KEY: misc_feature
21 LOCATION: (26)..(0)
22 OTHER INFORMATION: 1 of 2 allelic variants (17700 is other entry)
23 NAME/KEY: misc_feature
24 LOCATION: (25)..(26)
25 OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
26 NAME/KEY: misc_feature
27 LOCATION: (0)..(0)
28 OTHER INFORMATION: Accession number CG43932310
29 US-09-755-374A-17699

```

	Query Match	0.6%	Score 23.8:	DB 29;	Length 50;
	Best Local Similarity	72.1%:	Pred. No.2.8e+05;		
	Matches 31; Conservative	0;	Mismatches 12;	Indels	0;
Gy	3470	tcttcgcatttttctcctaattactactattatgatgtatt	3512		
db	7	tttttttttttttttttttgacactagatttatgacatttatt	49		

```

RESULT 36
US-09-396-196F-83096
; Sequence 83096, Application US/09396196F
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196F
CURRENT FILING DATE: 2001-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 83096
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196F-83096

```

Query Match	0.6%	Score 23.4	DB 17	Length 25
Best local similarity	96.0%	Pred. No. 2.5e+05		
Matches 24	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY 2110	agcccttgccccagcgaatgctgaat	2134		
db 1	agcccttgccccagcgaatgctgaat	25		

```

1  RESULT 7
2  US-08-401-791A-15261
3  ; Sequence 15261, Application US/08401791A
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Haseltine, William
6  ; APPLICANT: Rosen, Craig
7  ; APPLICANT: Ruben, Steve
8  ; APPLICANT: Dillon, Patrick
9  ; APPLICANT: Li, Haodong
10 ; APPLICANT: Earle-Hughes, Julie
11 ; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
12 ; NUMBER OF SEQUENCES: 17621
13 ; CORRESPONDENCE ADDRESS:
14 ; ADDRESSEE: Carella, Byrne, Bain, Gillfillan, Cecchi, Stewart, & Olsteln
15 ; STREET: 6 Becker Farm Road
16 ; CITY: Roseland
17 ; STATE: New Jersey
18 ; COUNTRY: USA
19 ; ZIP: 07068
20 ;
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
23 ; COMPUTER: HP Vectra 486/33
24 ; OPERATING SYSTEM: MSDOS version 5.0
25 ; SOFTWARE: ASCII Text
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08/401,791A
28 ; FILING DATE:
29 ; CLASSIFICATION: 435
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER:
32 ; FILING DATE:
33 ; ATTORNEY/AGENT INFORMATION:
34 ; NAME: Olsteln, Elliot
35 ; REGISTRATION NUMBER: 24,025
36 ; REFERENCE/DOCKET NUMBER: 325800-307
37 ; TELECOMMUNICATION INFORMATION:
38 ; TELEPHONE: (201) 994-1700
39 ; TELEFAX: (201) 994-1744
40 ; INFORMATION FOR SRO ID NO: 15261:
41 ; SEQUENCE CHARACTERISTICS:
42 ; LENGTH: 50 base pairs
43 ;

```



```

RESULT 11
PCT-US01-47856-5024/C
; Sequence 5024, Application PC/TUS0147856
; GENERAL INFORMATION:
; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Quertemous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 506612000140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5024
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47856-5024

Query Match      0.6%; Score 23.2; DB 1; Length 50;
Best Local Similarity 70.5%; Pred. No. 4e+05;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Cy 1214 gactcttacaagaacatcccgatggtcttttttgatgctga 1237
          ||| | | | | | | | | | | | | | | | | | | |
Db    44 GAATGCTTATAAGAAATCTCAAAAAGGTATTGTGGTGCGAGA 1

RESULT 12
US-09-755-374A-6837/C
; Sequence 6837, Application US/09755374A
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Met
; TITLE OF INVENTION: Use Theoret
; FILE REFERENCE: 15866-611
; CURRENT APPLICATION NUMBER: US/09/755,374A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/174962
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 6837
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 1 of 2 allelic variants (6838 is other entry)
; NAME/KEY: misc_feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number C94911096
US-09-755-374A-6837

```

```

Query Match Similarity      0.6%; Score 23.2; DB 29; Length 50;
Best Local Similarity       77.8%; Pred. No. 4e+05; Indels      0; Gaps      0;
Matches    28; Conservative 0; Mismatches   8;

QY    2555 ccacctccagcttcttccttttctgttaataaaaga 2590
      ||| |||| | | | | | | | | | | | | | | | | |
Db     44 CCAACCCAGATTGTACTTTTCTTTTCCTAA 9

RESULT 13
US-09-755-374A-13433
; Sequence 13433, Application US/09755374A
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and M
; FILE REFERENCE: 15966-611
; CURRENT APPLICATION NUMBER: US/09/755,374A
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/174962
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 13433
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (26)..(0)
; OTHER INFORMATION: 1 of 2 allelic variants (13434 is other entry)
; NAME/KEY: misc-feature
; LOCATION: (25)..(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; NAME/KEY: misc-feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Accession number cg44002450
US-09-755-374A-13433

Query Match          0.6%; Score 23.2; DB 29; Length 50;
Best Local Similarity 77.8%; Pred. No. 4e+05; Indels      0; Gaps      0;
Matches    28; Conservative 0; Mismatches   8;

QY    2563 cagcttctctccttttttttctgaaaaaaga 2598
      |||||| | | | | | | | | | | | | | | | |
Db     15 cagctttttttttttttttaataaaaaga 50

RESULT 14
US-08-346-731-6670
; Sequence 6670, Application US/08346731
; GENERAL INFORMATION:
; APPLICANT: Craig A. Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - P016
; NUMBER OF SEQUENCES: 12477
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,731
; FILING DATE:
; CLASSIFICATION: 435

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER:
3 FILING DATE:
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Benson, Bob
6 REGISTRATION NUMBER: 30,446
7 REFERENCE/DOCKET NUMBER: P01
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (301) 309-8504
10 TELEFAX: (301) 309-8512
11 INFORMATION FOR SEQ ID NO: 6670:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 50 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: double
16 TOPOLOGY: linear
17
18 US-08-346-731-6670

Query Match	0.6%	Score 23	DB 7	Length 50
Best Local Similarity	66.7%	Pred. No.	4.6e+05	
Matches 32, Conservative		Mismatches	16	Indels 0; Gaps 0.

```
QY      2556 caccctccagcattcttccttctttttttctgaaaaaaggaaaag   2603
          ||    |||  |  |  ||||| |||  |
Db       3 CANAGCCCTTTTTTTT TTTTTTTT TTTTA AAAAAA AAAAGG   50
```

RESULT 15
US-08-420-856-6670
Sequence 6670 Application US/08420856

```

1  APPLICANT:  Rosen, Craig A.
2  APPLICANT:  Ruben, Steve M.
3  APPLICANT:  Dillon, Patrick J.
4  APPLICANT:  Li, Haodong
5  APPLICANT:  Haseltine, William A.
6  TITLE OF INVENTION:  Human Genes, Sequences, and Expression Products - 16
7  NUMBER OF SEQUENCES:  12477
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, & Olstein
10 STREET:  6 Becker Farm Road
11 CITY:  Roseland
12 STATE:  New Jersey
13 COUNTRY:  USA
14 ZIP:  07068
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE:  Diskette, 3.50 inch, 1.4MB storage
18 COMPUTER:  HP Vectra 486/33
19 OPERATING SYSTEM:  MSDOS version 5.0
20 SOFTWARE:  ASCII Text
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER:  US/08/420,856
24 FILING DATE:
25 CLASSIFICATION:  536
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER:
28 FILING DATE:
29 ATTORNEY/AGENT INFORMATION:
30 NAME:  Olstein, Elliot
31 REGISTRATION NUMBER:  24,025
32 REFERENCE/DOCKET NUMBER:  325800-259
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE:  (201) 994-1700
35 TELEFAX:  (201) 994-1744
36 INFORMATION FOR SEQ. ID NO.:  6670:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH:  50 base pairs
39 TYPE:  nucleic acid
40 STRANDEDNESS:  double
41 TOPOLOGY:  linear
42
43 US-08-420-856-6670

```

	Query Match	0.6%	Score 23:	DB 8:	Length 50;
	Best Local Similarity	66.7%	Pred.	4.6e+05;	
	Matches 37; Conservative	0;	Mismatches 16;	Indels 0;	Gaps 0;
Oy	2556 caactccacagcttcctcctcttttcttgataaaagaagaag	2603			
Db	3 CANAGCCCTTTTITTTTTTTTTTTTTTTTAAAAAAAAGAAG	50			

Search completed: September 18, 2002, 02:37:20
Job time: 9827 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 23:59:13 : Search time 655.22 Seconds
(without alignments)
18027.320 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attaacagcgctgttagt.....aaacttaagtattatta 3713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2122332 seqs, 1590608744 residues
Total number of hits satisfying chosen parameters: 1036418

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23.4	0.6	25	US-09-396-196G-83096	Sequence 83096, A
2	23.2	0.6	50	US-10-131-831-5024	Sequence 5024, Ap
3	22.6	0.6	45	US-10-189-360-50	Sequence 50, Appl
4	22.4	0.6	25	US-09-396-196G-83095	Sequence 83095, A
5	22.2	0.6	50	US-10-131-831-7656	Sequence 7656, Ap
6	21.8	0.6	25	US-09-396-196G-83082	Sequence 83082, A
7	21.8	0.6	25	US-09-396-196G-83089	Sequence 83089, A
8	21.6	0.6	50	US-10-131-831-4391	Sequence 4391, Ap
9	21.4	0.6	43	US-10-027-632-177610	Sequence 177610, Ap
10	21.4	0.6	43	US-10-027-632-177620	Sequence 177620, Ap
11	21.4	0.6	50	US-10-131-831-4588	Sequence 4588, Ap
12	21.2	0.6	46	US-10-055-728-32	Sequence 32, Appl
13	21	0.6	43	US-10-027-632-177600	Sequence 177600, Ap
14	21	0.6	47	US-10-170-097-805	Sequence 805, App
15	21	0.6	48	US-10-156-306-7691	Sequence 7691, Ap
16	21	0.6	50	US-10-131-831-2704	Sequence 2704, Ap
17	21	0.6	50	US-10-131-831-3010	Sequence 3010, Ap
18	21	0.6	50	US-10-131-831-3861	Sequence 3861, Ap
19	20.6	0.6	40	US-09-914-101-10	Sequence 10, Appl
20	20.6	0.6	50	US-09-718-321A-50	Sequence 50, Appl
21	20.4	0.5	44	US-10-027-632-75768	Sequence 75768, A
22	20.4	0.5	46	US-10-170-097-1292	Sequence 1292, Ap
23	20.4	0.5	48	US-09-745-237A-4329	Sequence 4329, Ap
24	20.4	0.5	50	US-09-923-070A-6	Sequence 6, Appl1
25	20.4	0.5	50	US-09-724-379A-6	Sequence 6, Appl1

C	26	20.4	0.5	50	6	US-10-131-831-391	Sequence 391, App
	27	20.2	0.5	25	5	US-09-396-196G-83088	Sequence 83088, A
	28	20.2	0.5	25	5	US-09-396-196G-83097	Sequence 83097, A
C	29	20.2	0.5	25	5	US-09-396-196G-92147	Sequence 92147, A
C	30	20.2	0.5	36	4	US-08-705-477E-68	Sequence 68, Appl
C	31	20.2	0.5	47	5	US-09-702-498A-23	Sequence 23, Appl
C	32	20.2	0.5	47	5	US-09-702-498A-24	Sequence 24, Appl
C	33	20.2	0.5	47	7	US-10-170-097-1167	Sequence 1167, Ap
C	34	20.2	0.5	48	5	US-09-730-289B-1167	Sequence 1167, Ap
C	35	20.2	0.5	48	7	US-10-156-306-7112	Sequence 7112, Ap
C	36	20.2	0.5	50	5	US-09-886-492-3196	Sequence 3196, Ap
C	37	20.2	0.5	50	6	US-10-131-831-3607	Sequence 3607, Ap
C	38	20.2	0.5	50	6	US-10-131-831-4502	Sequence 4502, Ap
C	39	20.2	0.5	50	7	US-10-097-105-1012	Sequence 1012, Ap
C	40	20	0.5	40	4	US-08-961-083-245	Sequence 245, App
C	41	20	0.5	47	7	US-10-170-097-804	Sequence 804, App
C	42	20	0.5	48	5	US-09-730-289B-1326	Sequence 1326, Ap
C	43	20	0.5	48	5	US-09-503-138B-21	Sequence 21, Appl
C	44	20	0.5	48	7	US-10-150-407-21	Sequence 21, Appl
C	45	20	0.5	48	7	US-10-156-306-7182	Sequence 7182, Ap

ALIGNMENTS

```
RESULT 1
US-09-396-196G-83096
; Sequence 83096, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83096

Query Match      0.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 5e+04;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2110 agccctgcccagcaatgctgaat 2134
Db 1 agccctgcccagcaatgctgaat 25

RESULT 2
US-10-131-831-5024/c
; Sequence 5024, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
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; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5024
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-5024

Query Match
Best Local Similarity 70.5%; Pred. No. 7.4e+04;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1214 gactcttaacagacacccctgacgtcttcttttgatgactga 1257
Db 44 GAATGCTATFAGAAATCTCAAAAGGTATTGTGGTGCACAGA 1

RESULT 3
US-10-189-360-50
; Sequence 50, Application US/10189360
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; Sornowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS
; FOR THERAPE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEDD and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/189,360
; FILING DATE: 02-Jul-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Notlenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: (Seq4g1y)2
; LOCATION: 3..45
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-189-360-50

Query Match
Best Local Similarity 0.6%; Score 22.6; DB 6; Length 45;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 401 atggcgtgcgcctccctccggccgtctctgctgc 437
Db 3 ATGGCTCGTCGTGCGGCTGTGTCGTGCGGCG 39

RESULT 4
US-09-396-196G-83095
; Sequence 83095, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 83095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83095

Query Match
Best Local Similarity 0.6%; Score 22.4; DB 5; Length 25;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2057 agcctcagaagacctggaacaaga 2080
Db 2 agcctcagaagacctggaacaaga 25

RESULT 5
US-10-131-831-7656/C
; Sequence 7656, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7656
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-7656
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Query Match
Best Local Similarity 0.6%; Score 22; DB 6; Length 50;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1638 gagacactgtctcagtcacgcgccagct 1667
Db 48 GAGACAGGCTCTCACTGATATGCCAGGCT 19

RESULT 6
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10 TITLE OF INVENTION: Identification and Monitoring of

RESULT 12
US-10-055-728-32

QY 2939 ggttgctttctctaagtgaagacttaccaatgtaatt 2977
| | | | | | | | | : | | | | | | | |

Db 39 GCCTTTGTATGAGTGTGACRTTATACCTTGAAATTT 1

RESULT 14

US-10-170-097-805

; Sequence 805, Application US/10170097

; GENERAL INFORMATION:

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Bouqueleref, Lydie

; APPLICANT: Chumakov, Ilya

; APPLICANT: Cohen, Annick

; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

; FILE REFERENCE: GEN-T114XC2D1

; CURRENT APPLICATION NUMBER: US/10/170,097

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 09/641,638

; PRIOR FILING DATE: 2000-08-16

; PRIOR APPLICATION NUMBER: US 09/502,330

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: US 60/133,200

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: US 09/275,267

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: US 60/119,917

; PRIOR FILING DATE: 1999-02-12

; NUMBER OF SEQ ID NOS: 1304

; SOFTWARE: Patent.pm

; SEQ ID NO 805

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 24

; OTHER INFORMATION: 12-740-118 : polymorphic base C or T

US-10-170-097-805

Query Match

Best Local Similarity 0.6%; Score 21; DB 7; Length 47;

Matches 27; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Oy 948 tccacataaagaggggaatttcgcagagcgcttcca 988

||||| ||||| ||||| : ||||| ||||| |||||

Db 4 tccaccacaaaagryggaayctaaccagagagcttccaa 44

; RESULT 15

US-10-156-306-7691/C

; Sequence 7691, Application US/10156306

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: MCSwigen, James

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

; FILE REFERENCE: MBH01-664-A (400/050)

; CURRENT APPLICATION NUMBER: US/10/156,306

; CURRENT FILING DATE: 2002-05-28

; NUMBER OF SEQ ID NOS: 8013

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7691

; LENGTH: 48

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-156-306-7691

Oy 411 cctctccgggacgcgtcttcggtcgcgttttcaccttgatc 455

Db 46 CCTTCTCCCGGACGATGTCTTGAAGGAGTTTCTCTCTGCTC 2

Search completed: September 18, 2002, 02:48:37
Job time: 10164 sec

Query Match 0.6%; Score 21; DB 7; Length 48;
Best Local Similarity 66.7%; Pred. No. 2.6e+05;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
